

31-05-2000

Case number

PCT/GB99/00838

CLMS

30 May 2000

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Claims

1. An isolated mammalian sodium channel protein comprising
 - (i) The amino acid sequence shown in SEQ I.D No 2 or
 - (ii) A variant thereof which has at least 70% identity to the amino acid sequence of SEQ I.D. No 2.
2. A protein according to claim 1 wherein the variant has at least 90% identity to the amino acid sequence of SEQ I.D. No 2.
3. An isolated sodium channel protein according to claim 1 ~~or 2~~ which is a human protein.
4. An isolated sodium channel protein according to claim 1 which is derivable from the dorsal root ganglion of a mammal and which has an IC₅₀ for TTX of about 1 μ M.
5. An isolated nucleotide sequence encoding a sodium channel protein or variant thereof according to ~~any one of claims 1 to 4.~~ ^{claim 1}
6. An isolated nucleotide sequence according to claim 5 which is a DNA sequence.
7. An isolated nucleotide sequence according to claim 5 which comprises:
 - (a) the nucleic acid sequence of SEQ ID NO 1 and/or a sequence complementary thereto; or
 - (b) a sequence which hybridises under stringent conditions to a sequence as defined in (a); or
 - (c) a sequence that is degenerate as a result of the genetic code to a sequence as defined in (a) or (b); or
 - (d) a sequence having at least 70% identity to a sequence as defined in (a), (b) or (c).
8. A recombinant polynucleotide which comprises:

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- 5 (a) one or more of the nucleotide sequences of SEQ ID NO 3 to 17 and/or a sequence complementary thereto; or
- (b) a sequence which hybridises under stringent conditions to a sequence as defined in (a); or
- (c) a sequence that is degenerate as a result of the genetic code to a sequence as defined in (a) or (b); or
- (d) a sequence having at least 70% identity to a sequence as defined in (a), (b) or (c).
- 10 9. A recombinant polynucleotide according to claim 8 which comprises all of the sequences as defined in SEQ ID 3 to 17 wherein ascending numerical order represents the order in which the SEQ ID is read in the 5' to 3' direction
- 15 10. An isolated amino acid sequence encoded for by a nucleotide according to claim 8 ~~or 9~~.
- 20 11. An expression vector comprising a polynucleotide according to ~~any one of claims 5 to 9~~ ^{claim 5}.
13. A host cell comprising an expression vector according to claim 11.
13. An antibody or fragment thereof which recognises and binds to a polypeptide according to ~~any one of claims 1 to 4~~ ^{claim 1}.
- 25 14. An isolated polypeptide according to ~~any one of claims 1 to 4~~ ^{claim 1} for use in a method of screening for agents with analgesic or anti-hypersensitivity activity.
- 30 15. A method for the identification of a modulator of a sodium channel protein according to ~~any one of claims 1 to 4~~ ^{claim 1}, comprising contacting said protein with a test compound and detecting changes in the activity of the sodium channel protein due to the test compound.
16. A method of determining whether a test compound is a modulator of sodium flux which method comprises expressing a protein according to ~~any one of~~ ^{claim 1}.

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a ~~claims 1-4~~ in a host cell; contacting said protein with a test compound; and measuring sodium flux.

5 17. A modulator identifiable by a method according to claim 15 ~~or 16~~, for use in therapy.

a 18. Use of a modulator indentifiable by a method as claimed in claim 15 ~~or 16~~ for the manufacture of an analgesic or anti-hypersensitivity medicament.

10 19. A method of treating a disorder which is responsive to modulation of a protein according to ~~any one of claims 1 to 4~~ ^{claim 1} which method comprises administering to a patient an effective amount of a modulator, identifiable by a method according to claim 15 ~~or 16~~.

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Team leader
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1 GGAGCCATAC GGTGCCCTGA TCCTCTGTAC CAGGAAGACA GGGTGAAGAT
5
51 GGAGGAGAGG TACTACCCGG TGATCTTCCC GGACGAGCGG AATTTCGCGC
101 CCTTCACTTC CGACTCTCTG GCTGCCATAA AGAAGCGGAT TGCTATCCAA
10
151 AAGGAGAGGA AGAAGTCCAA AGACAAGGCG GCAGCTGAGC CCCAGCCTCG
201 GCCTCAGCTT GACCTAAAGG CCTCCAGGAA GTTACCTAAG CTTTATGGTG
251 ACATTCCCCC TGAGCTTGTT ACGAAACCTC TGGAGGACCT GGACCCCTAC
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301 TACAAAGACC ATAAGACATT CATGGTGTTG AACAAGAAAA GAACAATTTA
351 TCGCTTCAGC GCCAAGCGGG CCTTGTTTAT TCTGGGGCCT TTTAATCCCC
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401 TCAGAAGCTT AATGATTCTG ATCTCTGTCC ATTCAGTCTT TAGCATGTTC
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601 TTTTCCTTCC TCCGAGATCC GTGGAACTGG CTGGACTTCA TTGTCAATTGG
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651 AACAGCGATC GCAACTTGTT TTCCGGGCAG CCAAGTCAAT CTTTCAGCTC
701 TTCGTACCTT CCGAGTGTTT AGAGCTCTGA AGGCGATTTC AGTTATCTCA
751 GGTCTGAAGG TCATCGTAGG TGCCCTGCTG CGCTCGGTGA AGAAGCTGGT
35
801 AGACGTGATG GTCCTCACTC TCTTCTGCCT CAGCATCTTT GCCCTGGTCG

851 GTCAGCAGCT GTTCATGGGA ATTCTGAACC AGAAGTGTAT TAAGCACAAC
901 TGTGGCCCCA ACCCTGCATC CAACAAGGAT TGCTTTGAAA AGGAAAAAGA
5 951 TAGCGAAGAC TTCATAATGT GTGGTACCTG GCTCGGCAGC AGACCCTGTC
1001 CCAATGGTTC TACGTGCGAT AAAACCACAT TGAACCCAGA CAATAATTAT
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15 1201 TACCTGCTTA ACCTAACCTT GGCTGTTGTC ACCATGGCTT ATGAAGAACA
1251 GAACAGAAAT GTAGCTGCTG AGACAGAGGC CAAGGAGAAA ATGTTTCAGG
1301 AAGCCCAGCA GCTGTTAAGG GAGGAGAAGG AGGCTCTGGT TGCCATGGGA
20 1351 ATTGACAGAA GTTCCCTTAA TTCCCTTCAA GCTTCATCCT TTTCCCGAA
1401 GAAGAGGAAG TTTTTCGGTA GTAAGACAAG AAAGTCCTTC TTTATGAGAG
25 1451 GGTCCAAGAC GGCCCAAGCC TCAGCGTCTG ATTCAGAGGA CGATGCCTCT
1501 AAAAATCCAC AGCTCCTTGA GCAGACCAAA CGACTGTCCC AGAACTTGCC
1551 AGTGGATCTC TTTGATGAGC ACGTGGACCC CCTCCACAGG CAGAGAGCGC
30 1601 TGAGCGCTGT CAGTATCTTA ACCATCACCA TACAGGAACA AGAAAAATTC
1651 CAGGAGCCTT GTTTCCCATG TGGGAAAAAT TTGGCCTCTA AGTACCTGGT
35 1701 GTGGGACTGT AGCCCTCAGT GGCTGTGCAT AAAGAAGGTC CTGCGGACCA
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1801 AATACCGTTT TCTTAGCCGT GGAGCACCAC AACATGGATG ACAACTTAAA
1851 GACCATACTG AAAATAGGAA ACTGGGTTTT CACGGGAATT TTCATAGCGG
5 1901 AAATGTGTCT CAAGATCATC GCGCTCGACC CTTACCACTA CTTCCGGCAC
1951 GGCTGGAATG TTTTGGACAG CATCGTGGCC CTCCTGAGTC TCGCTGATGT
10 2001 GCTCTACAAC AACTGTCTG ATAACAATAG GTCTTTCTTG GCTTCCCTCA
2051 GAGTGCTGAG GGTCTTCAAG TTAGCCAAAT CCTGGCCCAC GTTAAACACT
2101 CTCATTAAGA TCATCGGCCA CTCCGTGGGC GCGCTTGGA ACCTGACTGT
15 2151 GGTCTGACT ATCGTGGTCT TCATCTTTTC TGTGGTGGGC ATGCGGCTCT
2201 TCGGCACCAA GTTTAACAAG ACCGCCTACG CCACCCAGGA GCGGCCCAGG
20 2251 CGGCGCTGGC ACATGGATAA TTTCTACCAC TCCTCCTGG TGGTGTTCCG
2301 CATCCTCTGT GGGGAATGGA TCGAGAACAT GTGGGGCTGC ATGCAGGATA
2351 TGGACGGCTC CCCGTTGTGC ATCATTGTCT TTGTCCTGAT AATGGTGATC
25 2401 GGGAAGCTTG TGGTGCTTAA CCTCTTCATT GCCTTGCTGC TCAATTCCTT
2451 CAGCAATGAG GAGAAGGATG GGAGCCTGGA AGGAGAGACC AGGAAAACCA
30 2501 AAGTGCAGCT AGCCCTGGAT CGGTTCCGCC GGGCCTTCTC CTTTCATGCTG
2551 CACGCTCTTC AGAGTTTTTG TTGCAAGAAA TGCAGGAGGA AAAACTCGCC
2601 AAAGCCAAAA GAGACAACAG AAAGCTTTGC TGGTGAGAAT AAAGACTCAA
35 2651 TCCTCCCGGA TCGAGGGCCC TGGAAGGAGT ATGATACAGA CATGGCTTTG

2701 TACTGAC AGGCCGGGGC TCCGCTGGCC CCACTCGCAG AGGTAGAGGA
2751 CGATGTGGAA TATTGTGGTG AAGGCGGTGC CCTACCCACC TCACAACATA
5 2801 GTGCTGGAGT TCAGGCCGGT GACCTCCCTC CAGAGACCAA GCAGCTCACT
2851 AGCCCGGATG ACCAAGGGGT TGAAATGGAA GTATTTTCTG AAGAAGATCT
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10 2951 TCTCGGAATG CAGCACAATT GACCTGAATG ATATCTTTAG AAATTTACAG
3001 AAAACAGTTT CCCCCAAAAA GCAGCCAGAT AGATGCTTTC CCAAGGGCCT
15 3051 TAGTTGTCAC TTTCTATGCC ACAAACAGA CAAGAGAAAG TCCCCCTGGG
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3251 TAAGGTGTAC CGATAATATT TTCACATTTA TTTTCCTCCT GGAAATGATC
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30 3451 GCGCTGTCCC AGTTTGAAGG AATGAAGGT GTCGTCTACG CCCTGATCAG
3501 CGCCATACCT GCCATTCTCA ATGTCTTGCT GGTCTGCCTC ATTTTCTGGC
35 3551 TCGTATTTTG TATCTTGGGA GTAAATTTAT TTTCTGGGAA GTTTGGAAGG
3601 TGCATTAACG GGACAGACAT AAATATGTAT TTGGATTTTA CCGAAGTTCC

5

3651 GAACCGAAGC CAATGTAACA TTAGTAATTA CTCGTGGAAG GTCCCGCAGG

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3801 GAAAGACGAG CAGCCGGACT TTGAGGCGAA CCTCTACGCG TATCTCTACT

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3851 TTGTGGTTTT TATCATCTTC GGCTCCTTCT TTACCCTGAA CCTCTTTATC

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15

3951 AGACATTTTT ATGACAGAAG AACAGAAGAA ATATTACAAT GCAATGAAAA

4001 AGTTAGGAAC CAAGAAACCT CAAAAGCCCA TCCAAGGCC CCTGAACAAA

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20

4101 CATTCTGGGT CTTATTGTCT TAAATATGAT TATCATGATG GCTGAATCTG

4151 CCGACCAGCC CAAAGATGTG AAGAAAACCT TTGATATCCT CAACATAGCC

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4201 TTCGTGGTCA TCTTTACCAT AGAGTGTCTC ATCAAAGTCT TTGCTTTGAG

4251 GCAACACTAC TTCACCAATG GCTGGAACCT ATTTGATTGT GTGGTCGTGG

4301 TTCTTTCTAT CATTAGTACC CTGGTTTCCC GCTTGGAGGA CAGTGACATT

30

4351 TCTTTCCCGC CCACGCTCTT CAGAGTCGTC CGCTTGGCTC GGATTGGTCG

4401 AATCCTCAGG CTGGTCCGGG CTGCCCAGGG AATCAGGACC CTCCTCTTTG

4451 CTTTGATGAT GTCTCTCCCC TCTCTCTTCA ACATCGGTCT GCTGCTCTTC

35

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5 4651 CTCCTCAACC CCATGCTGGA GGCAAAGAA CACTGCAACT CCTCCTCCCA
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10 4801 GAGAACTTCA ACACAGCCAC GGAGGAGAGC GAGGACCCTC TGGGAGAGGA
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15 4901 CGCAGTTCAT CCAGTATTCG GCCCTCTCTG ACTTTGCGGA CGCCCTGCCG
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25 5151 CGAGCCCATA GTCACCACCA CCAAGAGGAA GGAGGAGGAG CAAGGCGCCG
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30 5301 CTTGTCCAGC TTGGATGTGG CCAAGGTCAA GGTTACAAT GACTGAACCC
5351 TCATCTCCAC CCCTACCTCA CTGCCTCACA GCTTAGCCTC CAGCCTCTGG
35 5401 CGAGCAGGCG GCAGACTCAC TGAACACAGG CCGTTCGATC TGTGTTTTTG
5451 GCTGAACGAG GTGACAGGTT GGCGTCCATT TTAAATGAC TCTTGAAAAG

5501 ATTTTCATGTA GAGAGATGTT AGAAGGGACT GCAAAGGACA CCGACCATAA

5551 CGGAAGGCCT GGAGGACAGT CCAACTTACA TAAAGATGAG AAACAAGAAG

5

5601 GAAAGATCCC AGGAAAACCTT CAGATTGTGT TCTCAGTACA TTCCCCAATG

5651 TGTCTGTTCG GTGTTTTGAG TATGTGACCT GCCACATGTA GCTCTTTTTT

10

5701 GCATGTACGT CAAAACCCTG CAGTAAGTTA ATAGCTTGCT ACGGGTGTTT

5751 CTACCAGCAT CACAGAATTG GGTGTATGAC TCAAACCTAA AAGCATGACT

5801 CTGACTTGTC AGTCAGCACC CCGACTTTCA GACGCTCCAA TCTCTGTCCC

15

5851 AGGTGTCTAA CGAATAAATA GGTAAGAGAA AAAAAAAAAA AAAAAAA

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SEQ.No.2

5 -47 GGAGCCATACGGTGCCCTGATCCTCTGTACCAGGAAGACAGGGTGAAGATGGAGGAGAGG 12
1 M E E R 4

13 TACTACCCGGTGATCTTCCCGGACGAGCGGAATTTCCGCCCCCTTCACTTCCGACTCTCTG 72
5 Y Y P V I F P D E R N F R P F T S D S L 24

10 73 GCTGCCATAAAGAAGCGGATTGCTATCCAAAAGGAGAGGAAGAAGTCCAAAGACAAGGCG 132
25 A A I K K R I A I Q K E R K K S K D K A 44

133 GCAGCTGAGCCCCAGCCTCGGCCTCAGCTTGACCTAAAGGCCTCCAGGAAGTTACCTAAG 192
15 45 A A E P Q P R P Q L D L K A S R K L P K 64

193 CTTTATGGTGACATTTCCCTGAGCTTGTTACGAAACCTCTGGAGGACCTGGACCCCTAC 252
65 L Y G D I P P E L V T K P L E D L D P Y 84

20 253 TACAAAGACCATAAGACATTCATGGTGTTGAACAAGAAAAGAACAATTTATCGCTTCAGC 312
85 Y K D H K T F M V L N K K R T I Y R F S 104

313 GCCAAGCGGGCCTTGTTCACTCTGGGGCCTTTTAATCCCCTCAGAAGCTTAATGATTTCGT 372
105 A K R A L F I L G P F N P L R S L M I R 124

25 373 ATCTCTGTCCATTCAGTCTTTAGCATGTTTCATCATCTGCACGGTGATCATCAACTGTATG 432
125 I S V H S V F S M F I I C T V I I N C M 144

433 TTCATGGCGAATTCTATGGAGAGAAGTTTCGACAACGACATTTCCGAATACGTCTTCATT 492
30 145 F M A N S M E R S F D N D I P E Y V F I 164

493 GGGATTTATATTTTAGAAGCTGTGATTAATATTGGCAAGAGGCTTCATTGTGGATGAG 552
165 G I Y I L E A V I K I L A R G F I V D E 184

35 553 TTTTCCTTCTCCGAGATCCGTGGAAGTGGCTGGACTTCATTGTTCATTGGAACAGCGATC 612
185 F S F L R D P W N W L D F I V I G T A I 204

613 GCAACTTGTTTTCCGGGACGCAAGTCAATCTTTCAGCTCTTCGTACCTTCCGAGTGTTT 672
205 A T C F P G S Q V N L S A L R T F R V F 224

40 673 AGAGCTCTGAAGGCGATTTTCAGTTATCTCAGGTCTGAAGGTCATCGTAGGTGCCCTGCTG 732
225 R A L K A I S V I S G L K V I V G A L L 244

733 CGCTCGGTGAAGAAGCTGGTAGACGTGATGGTCTCACTCTCTTCTGCCTCAGCATCTTT 792
45 245 R S V K K L V D V M V L T L F C L S I F 264

793 GCCCTGGTCGGTCAGCAGCTGTTTCATGGGAATTCTGAACCAGAAAGTGATTAAGCACAAAC 852
265 A L V G Q Q L F M G I L N Q K C I K H N 284

5 853 TGTGGCCCCAACCTGCATCCAACAAGGATTGCTTTGAAAAGGAAAAAGATAGCGAAGAC 912
285 C G P N P A S N K D C F E K E K D S E D 304

913 TTCATAATGTGTGGTACCTGGCTCGGCAGCAGACCCTGTCCCAATGGTTCTACGTGCGAT 972
305 F I M C G T W L G S R P C P N G S T C D 324

10 973 AAAACCACATTGAACCCAGACAATAATTATACAAAGTTTGACAACTTTGGCTGGTCCTTT 1032
325 K T T L N P D N N Y T K F D N F G W S F 344

1033 CTCGCCATGTTCCGGGTTATGACTCAAGACTCCTGGGAGAGGCTTTACCGACAGATCCTG 1092
15 345 L A M F R V M T Q D S W E R L Y R Q I L 364

1093 CGGACCTCTGGGATCTACTTTGTCTTCTTCTTCGTGGTGGTCATCTTCCTGGGCTCCTTC 1152
365 R T S G I Y F V F F F V V V I F L G S F 384

20 1153 TACCTGCTTAACCTAACCTGGCTGTTGTCACCATGGCTTATGAAGAACAGAACAGAAAT 1212
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1213 GTAGCTGCTGAGACAGAGGCCAAGGAGAAAAATGTTTCAGGAAGCCCAGCAGCTGTAAAGG 1272
405 V A A E T E A K E K M F Q E A Q Q L L R 424

25 1273 GAGGAGAAGGAGGCTCTGGTTGCCATGGGAATTGACAGAAGTTCCTTAATTCCCTTCAA 1332
425 E E K E A L V A M G I D R S S L N S L Q 444

1333 GCTTCATCCTTTTCCCCGAAGAAGAGGAAGTTTTCGGTAGTAAGACAAGAAAGTCCTTC 1392
30 445 A S S F S P K K R K F F G S K T R K S F 464

1393 TTTATGAGAGGGTCCAAGACGGCCCAAGCCTCAGCGTCTGATTCAGAGGACGATGCCTCT 1452
465 F M R G S K T A Q A S A S D S E D D A S 484

35 1453 AAAAAATCCACAGCTCCTTGAGCAGACCAAACGACTGTCCCAGAACTTGCCAGTGGATCTC 1512
485 K N P Q L L E Q T K R L S Q N L P V D L 504

1513 TTTGATGAGCACGTGGACCCCTCCACAGGCAGAGAGCGCTGAGCGCTGTCAGTATCTTA 1572
505 F D E H V D P L H R Q R A L S A V S I L 524

40 1573 ACCATCACCATACAGGAACAAGAAAAATTCAGGAGCCTTGTTTCCCATGTGGGAAAAAT 1632
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1633 TTGGCCTCTAAGTACCTGGTGTGGGACTGTAGCCCTCAGTGGCTGTGCATAAAGAAGGTC 1692
45 545 L A S K Y L V W D C S P Q W L C I K K V 564

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5 1813 AAAATAGGAACTGGGTTTTACGGGAATTTTCATAGCGGAAATGTGTCTCAAGATCATC 1872
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1933 CTCCTGAGTCTCGCTGATGTGCTCTACAACACACTGTCTGATAACAATAGGTCTTTCTTG 1992
645 L L S L A D V L Y N T L S D N N R S F L 664

15 1993 GCTTCCCTCAGAGTGCTGAGGGTCTTCAAGTTAGCCAAATCCTGGCCCACGTAAACACT 2052
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20 2113 ATCGTGGTCTTCATCTTTTCTGTGGTGGGCATGCGGCTCTTCGGCACCAAGTTTAACAAG 2172
705 I V V F I F S V V G M R L F G T K F N K 724

2173 ACCGCCTACGCCACCCAGGAGCGGCCAGGCGCGCTGGCACATGGATAATTTCTACCAC 2232
25 725 T A Y A T Q E R P R R R W H M D N F Y H 744

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30 2293 ATGCAGGATATGGACGGCTCCCCGTGTGCATCATTGTCTTTGTCCTGATAATGGTGATC 2352
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2353 GGGAAAGCTTGTGGTGCTTAACCTCTTCATTGCCTTGCTGCTCAATTCCTTCAGCAATGAG 2412
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35 2413 GAGAAGGATGGGAGCCTGGAAGGAGAGACCAGGAAAACCAAAGTGCAGCTAGCCCTGGAT 2472
805 E K D G S L E G E T R K T K V Q L A L D 824

2473 CGGTTCCGCCGGGCTTCTCCTTCATGTGTCACGCTCTTCAGAGTTTTTGTGCAAGAAA 2532
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2533 TGCAGGAGGAAAACTCGCCAAAGCCAAAAGAGACAACAGAAAGCTTTGCTGGTGAGAAT 2592
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45 2593 AAAGACTCAATCCTCCCGGATGCGAGGCCCTGGAAGGAGTATGATACAGACATGGCTTTG 2652
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5 2713 TATTGTGGTGAAGGCGGTGCCCTACCCACCTCACAACATAGTGCTGGAGTTCAGGCCGGT 2772
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2773 GACCTCCCTCCAGAGACCAAGCAGCTCACTAGCCCGGATGACCAAGGGGTGAAATGGAA 2832
925 D L P P E T K Q L T S P D D Q G V E M E 944

10 2833 GTATTTTCTGAAGAAGATCTGCATTTAAGCATACAGATCCTCGAAAGAAGTCTGACGCA 2892
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2893 GTGAGCATGCTCTCGGAATGCAGCACAATTGACCTGAATGATATCTTTAGAAATTTACAG 2952
965 V S M L S E C S T I D L N D I F R N L Q 984

15 2953 AAAACAGTTTCCCCCAAAAAGCAGCCAGATAGATGCTTTCCCAAGGGCCTTAGTTGTCAC 3012
985 K T V S P K K Q P D R C F P K G L S C H 1004

20 3013 TTTCTATGCCACAAAACAGACAAGAGAAAGTCCCCCTGGGTCTGTGGTGAACATTCCG 3072
1005 F L C H K T D K R K S P W V L W W N I R 1024

3073 AAAACCTGCTACCAAATCGTGAAGCACAGCTGGTTTGAGAGTTTCATAATCTTTGTTATT 3132
1025 K T C Y Q I V K H S W F E S F I I F V I 1044

25 3133 CTGCTGAGCAGTGGAGCGCTGATATTTGAAGATGTCAATCTCCCCAGCCGGCCCCAAGTT 3192
1045 L L S S G A L I F E D V N L P S R P Q V 1064

3193 GAGAAATTACTAAGGTGTACCGATAATATTTTCACATTTATTTTCCTCCTGGAAATGATC 3252
1065 E K L L R C T D N I F T F I F L L E M I 1084

30 3253 CTGAAGTGGGTGGCCTTTGGATTCCGGAGGTATTTACCAGTGCCTGGTGCTGGCTTGAT 3312
1085 L K W V A F G F R R Y F T S A W C W L D 1104

35 3313 TTCCTCATTTGGTGGTGTCTGTGCTCAGTCTCATGAATCTACCAAGCTTGAAGTCCTTC 3372
1105 F L I V V V S V L S L M N L P S L K S F 1124

3373 CGGACTCTGCGGGCCCTGAGACCTCTGCGGGCGCTGTCCCAGTTTGAAGGAATGAAGGTT 3432
1125 R T L R A L R P L R A L S Q F E G M K V 1144

40 3433 GTCGTCTACGCCCTGATCAGCGCCATACCTGCCATTCTCAATGTCTTGCTGGTCTGCCTC 3492
1145 V V Y A L I S A I P A I L N V L L V C L 1164

3493 ATTTTCTGGCTCGTATTTTGTATCTTGGGAGTAAATTTATTTTCTGGGAAGTTTGAAGG 3552
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45 3553 TGCATTAACGGGACAGACATAAATATGTATTTGGATTTTACCGAAGTTCCGAACCGAAGC 3612
1185 C I N G T D I N M Y L D F T E V P N R S 1204

3613 CAATGTAACATTAGTAATTACTCGTGGAAGGTCCCGCAGGTCAACTTTGACAACGTGGGG 3672
1205 Q C N I S N Y S W K V P Q V N F D N V G 1224

5 3673 AATGCCTATCTCGCCCTGCTGCAAGTGGCAACCTATAAGGGCTGGCTGGAAATCATGAAT 3732
1225 N A Y L A L L Q V A T Y K G W L E I M N 1244

3733 GCTGCTGTGCGATTCCAGAGAGAAAAGACGAGCAGCCGGACTTTGAGGCGAACCTCTACGCG 3792
1245 A A V D S R E K D E Q P D F E A N L Y A 1264

10 3793 TATCTCTACTTTGTGGTTTTTATCATCTTCGGCTCCTTCTTTACCCTGAACCTCTTTATC 3852
1265 Y L Y F V V F I I F G S F F T L N L F I 1284

15 3853 GGTGTTATTATTGACAACCTCAATCAGCAGCAGAAAAAGTTAGGTGGCCAAGACATTTTT 3912
1285 G V I I D N F N Q Q Q K K L G G Q D I F 1304

3913 ATGACAGAAGAACAGAAGAAATATTACAATGCAATGAAAAAGTTAGGAACCAAGAAACCT 3972
1305 M T E E Q K K Y Y N A M K K L G T K K P 1324

20 3973 CAAAAGCCCATCCCAAGGCCCTGAACAAATGTCAAGCCTTTGTGTTGACCTGGTCACA 4032
1325 Q K P I P R P L N K C Q A F V F D L V T 1344

4033 AGCCAGGTCTTTGACGTCATCATTCTGGGTCTTATTGTCTTAAATATGATTATCATGATG 4092
1345 S Q V F D V I I L G L I V L N M I I M M 1364

25 4093 GCTGAATCTGCCGACCAGCCCAAAGATGTGAAGAAAACCTTTGATATCCTCAACATAGCC 4152
1365 A E S A D Q P K D V K K T F D I L N I A 1384

30 4153 TTCGTGGTCATCTTTACCATAGAGTGTCTCATCAAAGTCTTTGCTTTGAGGCAACACTAC 4212
1385 F V V I F T I E C L I K V F A L R Q H Y 1404

4213 TTCACCAATGGCTGGAACCTTATTGATTGTGTGGTCTGTTCTTTCTATCATTAGTACC 4272
1405 F T N G W N L F D C V V V V L S I I S T 1424

35 4273 CTGGTTTCCCGCTTGGAGGACAGTGACATTTCTTTCCCGCCCACGCTCTTCAGAGTCGTC 4332
1425 L V S R L E D S D I S F P P T L F R V V 1444

4333 CGCTTGGCTCGGATTGGTCGAATCCTCAGGCTGGTCCGGGCTGCCCGGGGAATCAGGACC 4392
1445 R L A R I G R I L R L V R A A R G I R T 1464

40 4393 CTCCTCTTTGCTTTGATGATGTCTCTCCCTCTCTCTTCAACATCGGTCTGCTGCTCTTC 4452
1465 L L F A L M M S L P S L F N I G L L L F 1484

45 4453 CTGGTGATGTTTCAATTTACGCCATCTTTGGGATGAGCTGGTTTTCCAAAGTGAAGAAGGGC 4512
1485 L V M F I Y A I F G M S W F S K V K K G 1504

4513 TCCGGGATCGACGACATCTTCAACTTCGAGACCTTTACGGGCAGCATGCTGTGCCTCTTC 4572

1505 S G I D D I F N F E T F T G S M L C L F 1524

4573 CAGATAACCACTTCGGCTGGCTGGGATACCTCCTCAACCCCATGCTGGAGGCAAAAGAA 4632
1525 Q I T T S A G W D T L L N P M L E A K E 1544

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4633 CACTGCAACTCCTCCTCCCAAGACAGCTGTCAGCAGCCGCAGATAGCCGTCGTCTACTTC 4692
1545 H C N S S S Q D S C Q Q P Q I A V V Y F 1564

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4693 GTCAGTTACATCATCATCTCCTTCTCATCGTGGTCAACATGTACATCGCTGTGATCCTC 4752
1565 V S Y I I I S F L I V V N M Y I A V I L 1584

4753 GAGAACTTCAACACAGCCACGGAGGAGAGCGAGGACCTCTGGGAGAGGACGACTTTGAA 4812
1585 E N F N T A T E E S E D P L G E D D F E 1604

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4813 ATCTTCTATGAGGTCTGGGAGAAGTTTGACCCCGAGGCGTCGCAGTTCATCCAGTATTCG 4872
1605 I F Y E V W E K F D P E A S Q F I Q Y S 1624

4873 GCCCTCTCTGACTTTGCGGACGCCCTGCCGAGCCGTTGCGTGTGGCCAAGCCGAATAAG 4932
1625 A L S D F A D A L P E P L R V A K P N K 1644

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4933 TTTCAGTTTCTAGTGATGGACTTGCCCATGGTGATGGGCGACCGCCTCCATTGCATGGAT 4992
1645 F Q F L V M D L P M V M G D R L H C M D 1664

4993 GTTCTCTTTGCTTTCACTACCAGGGTCCTCGGGGACTCCAGCGGCTTGGATACCATGAAA 5052
1665 V L F A F T T R V L G D S S G L D T M K 1684

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5053 ACCATGATGGAGGAGAAGTTTATGGAGGCCAACCTTTTAAGAAGCTCTACGAGCCCATA 5112
1685 T M M E E K F M E A N P F K K L Y E P I 1704

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5113 GTCACCACCACCAAGAGGAAGGAGGAGGAGCAAGGCGCCGCCGTCATCCAGAGGGCCTAC 5172
1705 V T T T K R K E E E Q G A A V I Q R A Y 1724

5173 CGGAAACACATGGAGAAGATGGTCAAACCTGAGGCTGAAGGACAGGTCAAGTTCATCGCAC 5232
1725 R K H M E K M V K L R L K D R S S S S H 1744

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5233 CAGGTGTTTTGCAATGGAGACTTGTCAGCTTGGATGTGGCCAAGGTCAAGGTTTACAAT 5292
1745 Q V F C N G D L S S L D V A K V K V H N 1764

5293 GACTGAACCTCATCTCCACCCCTACCTCACTGCCTCACAGCTTAGCCTCCAGCCTCTGG 5352
1765 D • 1766

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5353 CGAGCAGGCGGCAGACTCACTGAACACAGGCCGTTTCGATCTGTGTTTTTGGCTGAACGAG 5412

5413 GTGACAGGTTGGCGTCCATTTTTAAATGACTCTTGGAAGATTTCATGTAGAGAGATGTT 5472

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5473 AGAAGGGACTGCAAAGGACACCGACCATAACGGAAGGCCTGGAGGACAGTCCAACCTTACA 5532

5533 TAAAGATGAGAAACAAGAAGGAAAGATCCCAGGAAACTTCAGATTGTGTTCTCAGTACA 5592
5593 TTCCCAATGTGTCTGTTCGGTGTGTTTGTAGTATGTGACCTGCCACATGTAGCTCTTTTTT 5652
5 5653 GCATGTACGTCAAAACCCTGCAGTAAGTTAATAGCTTGCTACGGGTGTTCCCTACCAGCAT 5712
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10 5833 AAAAAAAAAAAAAAAAAA 5849

Human SNS_{2A} sequences**SEQ.I.D.NO:3**

5 ATCCTAGGGCAGGCTGTTTTATTCCCGCCTCCTGAGGCCTTTCTGAGGATCTGTGGCTTG
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10 AAAAGGAGAAAAAGAAGTCTAAAGACCAGACAGGAGAAGTACCCCAGCCTCAACCTCAG
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SEQ.I.D.NO.4

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SEQ.I.D.NO.5

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SEQ.I.D.NO.8

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SEQ.I.D.No.9

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50 CACTCCTTCCTAGTGGTATCGCGCATCCTCTTGCG

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5 CAGACAATGAGAACTCCGTACTACTATGGTGAAAGAAGGTCTTAGTAAAAGGCACCCCC
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SEQ.I.D.NO.12

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15 GAATGAAGGTACATTCTGCAGAAGAATGGGTAGAAGTTCAGTTAACAGAGAAAGGTGGA
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SEQ.I.D.NO.13

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25 TTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCTTTTCTGGAAAATTTGGGAA
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SEQ.I.D.NO.14

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CCTA

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SEQ.I.D.NO.15

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45 GGTGTCTTGATTGGTAATTGTATCTCTGTCTCCAAAGAAGGAATCC

SEQ.I.D.NO.16

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55 CAAAGCAGAAAACCTGGGCCAAGTGTACTTTCTGAAAGAATAGACAGGGGTACTAATGCCA
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SEQ.I.D.NO:17

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